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US-09-949-002-577
US-09-949-002-705
US-08-181-9118-1
US-09-382-552-59
US-08-781-420-9
US-08-781-420-9
US-08-874-102-9
US-08-874-102-9
US-08-874-102-9
US-08-94-919A-9
US-08-781-420-5
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US-08-984-919A-7
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US-09-986-595A-7
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ALIGNMENTS

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Sequence 1, Application US/09859724

Patent No. 6699843

GENERAL INFORMATION:

APPLICANT: Pietras, Kristian

APPLICANT: Pietras, Kristian

APPLICANT: Heldin, Carl Henrik

APPLICANT: Heldin, Carl Henrik

APPLICANT: Rubin, Kristofer

TITLE OF INVENTION: METHOD FOR TREATMENT OF TUMORS USING NUCLEIC ACID

TITLE OF INVENTION: LIGANDS TO PDGF

TITLE OF INVENTION: LIGANDS TO PDGF

FILE REFERENCE: NEX90

CURRENT FILING DATE: 2001-09-21

PRIOR APPLICATION NUMBER: 08/479,725

PRIOR PLILNG DATE: 1995-06-07

PRIOR PLILNG DATE: 1997-12-16

NUMBER OF SEQ ID NOS: 2

SOFTWARE: PatentIN Ver. 2.0

SEQ ID NO 1

LENGTH: 30

TYPE: DNA

ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: Wucleic Acid Ligand
NAME/KEX: modified base
LOCATION: (6). (30)
OTHER INFORMATION: 2 fluoro-2 decoxyuridine
NAME/KEX: modified base
LOCATION: (8). (20)
OTHER INFORMATION: 2 fluoro-2 decoxyuridine
NAME/KEX: modified base
LOCATION: (8). (20)
OTHER INFORMATION: 2 fluoro-2 decoxyuridine
NAME/KEX: modified base
LOCATION: (9). (31)
OTHER INFORMATION: 2 decoxyuridine
LOCATION: (9). (31)
OTHER INFORMATION: 2 decoxyuridine
LOCATION: (9). (31)
OTHER INFORMATION: 2 decoxyquanosine
NAME/KEX: modified base
LOCATION: (22)
                                          US-09-859-724-1
Sequence 1, Appli
Sequence 3, Appli
Sequence 11347, A
Sequence 11347, A
Sequence 10626, A
Sequence 2715, A
Sequence 2715, Ap
Sequence 1, Appli
Sequence 2284, Appli
Sequence 2284, Appli
Sequence 2284, Appli
Sequence 2284, Appli
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Sequence 44850, A
Sequence 44851, A
Sequence 73896, A
Sequence 193773,
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13029, A
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Sequence 24104, A
Sequence 8, Appli
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Sequence 13904, A
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                                                                                                      January 8, 2006, 15:39:24; Search time 101 Seconds (without alignments) 527.989 Million cell updates/sec
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1: /cgn2_6/ptodata/1/ina/1_COMB.seq:*

2: /cgn2_6/ptodata/1/ina/5_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/B_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/H_COMB.seq:*

6: /cgn2_6/ptodata/1/ina/PP_COMB.seq:*

7: /cgn2_6/ptodata/1/ina/PP_COMB.seq:*

8: /cgn2_6/ptodata/1/ina/PP_COMB.seq:*

9: /cgn2_6/ptodata/1/ina/PP_COMB.seq:*

9: /cgn2_6/ptodata/1/ina/RP_COMB.seq:*
           GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
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US-09-246-461-3
US-10-021-330-3
US-09-270-767-11347
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US-09-270-767-11347
US-09-270-767-11489
US-09-270-767-16423
US-09-489-016-16423
US-09-447-497-4
US-09-533-559-2284
US-09-533-559-2284
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US-09-533-559-2284
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US-09-949-016-14851
US-09-949-016-13904
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Maximum Match 100%
Listing first 45 summaries
                                                                        nucleic search, using sw model
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seq length: 200000000
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Match Length DB
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CURRENT APPLICATION NUMBER: US/10/021,330
CURRENT FILING DATE: 2001-12-10
PRIOR APPLICATION NUMBER: US/09/246,461
PRIOR FILING DATE: 1999-02-09
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PATENTIN Ver: 2.0
SEQ ID NO 3
LENGTH: 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 11347, Application US/09270767; Patent No. 6703491; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 84.6%;
Matches 22; Conservative
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US-09-270-767-11347
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OTHER INFORMATION: A at position 22 is 2'-O-Methyl-2'-deoxyadenosine
NAME/KEY: modified base
LOCATION: 10. (30)
OTHER INFORMATION: The residues at positions 9 and 10 are connected by a hexaethylen
OTHER INFORMATION: phosphoramidite linker. The residues at positions 21 and 22 are
OTHER INFORMATION: connected by a hexaethylene glycol phosphoramidite linker.
NAME/KEY: modified base
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Patent No. 6329145

GENERAL INFORMATION:
APPLICANT: Janjic, Nebojaa
APPLICANT: Gold, Larry
TITLE OF INVENTION: Aptamers as Reagents for high Throughput Screening
TITLE REFERENCE: NEX.8

CURRENT APPLICATION NUMBER: US/09/246,461

CURRENT FILING DATE: 1999-02-09

NUMBER OF SEQ ID NOS: 4

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 3

LENGTH: 31
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LOCATION: (1)..(31)
OTHER INFORMATION: The t at position 1 is 2'-NH2. The u's and c's at OTHER INFORMATION: positions 7, 9, 20, 21, 27, 28 and 29 are 2'-F.
OTHER INFORMATION: The a's and g's at positions 10, 15, 17, 22 and 30
OTHER INFORMATION: are 2'-O-methyl.
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NAME/KTY: modified base

NAME/KTY: modified base

CCATION: (1)..(31)

OTHER INFORMATION: The g at position 10 and the a at position 22 have

OTHER INFORMATION: been modified with polyethylene glycol of 18

CTHER INFORMATION: units.

US-09-246-461-3
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Patent No. 6670132
GENERAL INFORMATION:
APPLICANT: Janjic, Nebojsa
APPLICANT: Gold, Larry
TITLE OF INVENTION: Aptamers as Reagents for high Throughput Screening
                                                                                                                                                                                                                                                                                                                                                                             Gaps
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ORGANISM: Artificial Sequence
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US-09-246-461-3
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TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILLE REFERENCE: FILE RE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
OTHER INFORMATION: Description of Artificial Sequence: Nucleic acid OTHER INFORMATION: ligand
FRATURE:
NAME/KEY: modified base
LOCATION: (1)..(31)
OTHER INFORMATION: The t at position 1 is 2'-NH2. The u's and c's at OTHER INFORMATION: Positions 7, 9, 20, 21, 27, 28 and 29 are 2'-F.
OTHER INFORMATION: The a's and g's at positions 10, 15, 17, 22 and 30 OTHER INFORMATION: are 2'-O-methyl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: modified base LOCATION: (1)...(31) OTHER INFORMATION: The gat position 10 and the a at position 22 have OTHER INFORMATION: The modified with polyethylene glycol of 18 OTHER INFORMATION: units.
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Pred. No. 20;
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DB 3; Length 167708;

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US-09-489-039A-2715
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       Query Match
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APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

CURRENT APPLICATION NUMBER: 00/949,016

CURRENT PILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-0-09-08

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SEQ ID NO 16422
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APPLICANT: Homburger et al.

APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REPERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 10626
LENGTH: 705
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                                                                                                                                                                                                                                                                                           DB 3; Length 615;
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Best Local Similarity 84.6%; Pred. No. 21;
Matches 22; Conservative 0; Mismatches
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Best Local Similarity 84.6%; Pred. No. 21;
Matches 22; Conservative 0; Mismatches
                                                                                                                                                                                                                ) OTHER INFORMATION: n means any nucleotide US-09-270-767-14489
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SEQ TWARE: PatentIn Ver. 2.0
SEQ ID NO 14489
LENGTH: 615
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Patent No. 6812339
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; Sequence 10626, Application US/09270767
; Patent No. 6703491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-10626
                                                                                                                                                                    ORGANISM: Drosophila melanogaster
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US-09-949-016-16423
                                                                                                                                                  TYPE: DNA
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APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT PILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 2715
LENGTH: 603
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OTHER INFORMATION: mAIF-alt-exon-Gold
US-09-447-497-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 603;
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                                               IndelB
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APPLICANT: Riderovsi, David P.
APPLICANT: Siderovsi, David P.
APPLICANT: Siderovsi, David P.
APPLICANT: Susin, Santos A.
APPLICANT: Snow, Bryan E.L.
TITLE OF INVENTION: APOPTOSIS-INDUCING FACTOR FILE REFERENCE: 01017/36780
CURRENT APPLICATION NUMBER: US/09/447,497
CURRENT FILING DATE: 1999-11-23
EARLIER FILING DATE: 1999-11-23
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PATENTIN VOY: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 63.3%; Score 19; DB 3; Best Local Similarity 74.1%; Pred. No. 39; Matches 20; Conservative 2; Mismatches
65.3%; Score 19.6; I larity 73.1%; Pred. No. 65; Conservative 3; Mismatches
                                                                                                                      106 GGCGACAGCTGGAGCATCATGATCCTG 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 GGCUACGCGTAGAGCAUCATGATCCUG 29
                                                                                              5 CUACGCGTAGAGCAUCATGATCCUGT 30
                                                                                                                                                                                                                                      US-09-489-039A-2715
; Sequence 2715, Application US/09489039A
; Patent No. 6610836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-447-497-4
; Sequence 4, Application US/09447497
; Patent No. 6773911
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1875)
FEATURE:
                        Best Local Similarity
Matches 19; Conserv
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MOLECULE TYPE: DNA (genomic)
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 base pairs
                                           Query Match
Best Local Similarity 71.4
Matches 20; Conservative
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Matches 18; Conservative
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EDNESS: single
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STRANDEDNESS:
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US-09-270-767-8822
US-09-533-559-2284
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APPLICANT: Randy M. Berka
APPLICANT: Michael W. Rey
APPLICANT: Jeffrey R. Shuster
APPLICANT: Jeffrey R. Shuster
APPLICANT: Jeffrey R. Shuster
APPLICANT: Defrey Barke Olean
APPLICANT: Deter Bjarke Olean
TITLE OF INVENTION: Methods For Monitoring Multiple Gene;
TITLE OF INVENTION: Expression
FILE REFERENCE: 549-200-03
FILE REFERENCE: 549-200-03
FURRENT APPLICATION NUMBER: US/09/533,559
CURRENT FILING DATE: 2000-03-22
BARLIER FILING DATE: 1999-03-22
MUMBER FILING DATE: 1999-03-22
MUMBER FILING DATE: 1999-03-22
MUMBER FILING DATE: 1999-03-22
MUMBER FILING DATE: Mindows Version 4.0
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81.8%; Pred. No. 61;
:ive 2; Mismatches 2;
                                                                                                   RESULT 10

US-09-447-497-1

Sequence 1, Application US/09447497

Patent No. 6773911

GENERAL INFORMATION:

APPLICANT: Penninger, Josef M.

APPLICANT: Semer, Giddo P.

APPLICANT: Samcani, Naoufal

APPLICANT: Sancos A.

APPLICANT: Sow, Bryan E.L.

TITLE OF INVENTION: APPOPTOSIS-INDUCING FACTOR

FILE REFERENCE: 01017/36780

CURRENT APPLICATION NUMBER: US/09/447,497

CURRENT APPLICATION NUMBER: 06/109,595

EARLIER FILING DATE: 1999-11-23

NUMBER OF SEQ ID NOS: 25

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 1

LENGTH: 1932
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                                           1387 ceacracaccarcarcarcarc 1408
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US-09-533-559-2284
; Sequence 2284, Application US/09533559
; Patent No. 6902887
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  CGCGTAGAGCAUCATGATCCUG 29
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LOCATION: (1)...(485)
OTHER INFORMATION: n = A,T,C or G
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Best Local Similarity 81.8<sup>1</sup>
Matches 18, Conservative
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LOCATION: (1)..(1887)
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APPLICANT: SCHLOKAT, Uwe
APPLICANT: SCHLOKAT, Uwe
APPLICANT: FISCHER, Bernhard
APPLICANT: FISCHER, Bernhard
APPLICANT: FISCHER, Falko-Guenther
APPLICANT: Friedrich
APPLICANT: BIBL, Johann
TITLE OF INVENTION: A FUSION PROTEIN COMPRISING A FURIN
TITLE OF INVENTION: DERIVATIVE OR A DERIVATIVE OF A FURIN
TITLE OF INVENTION: BERIVATIVE OR A DERIVATIVE OF A FURIN
TITLE OF INVENTION: BARROLOGOUS SEQUENCE
TITLE
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                                                                                                       Gaps
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DB 3; Length 485;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/753,247
FILING DATE: 22-NOV-1996
CLASSIFICATION 1435
PRIOR APPLICATION DATE: 24-NOV-1995
ATTON NUMBER: 24-NOV-1995
ATTONENY/AGERT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
61.3%; Score 18.4; I 71.4%; Pred. No. 70; ive 2; Mismatches
                                                                                                                                                                                                                                                              181 AGGCAGCGTTTGGGGCATCATGATCCTG 208
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ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 7, Application US/08753247 Patent No. 6210929 GENERAL INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5390
TELEPAX: (202)672-5399
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Sequence 8, Application US/08753247

Sequence 8, Application US/08753247

Sequence 8, Application US/08753247

Sequence 8, Application US/08753247

SETION OF SEQUENCE

APPLICANT: BESTION OF SEQUENCE OF A DERIVATIVE OF A FURIN ANALOGUE AND A TITLE OF INVENTION: BERIVATIVE OR A DERIVATIVE OF A FURIN ANALOGUE AND A TITLE OF INVENTION: BERIVATIVE OR A DERIVATIVE OF A FURIN ANALOGUE AND A TITLE OF INVENTION: BERIVATIVE OR A DERIVATIVE OF A FURIN ANALOGUE AND A TITLE OF INVENTION: BETIVATIVE OR A DERIVATIVE OF A FURIN ANALOGUE AND A STREEP OF SEQUENCES:

ADDRESSEE: FOLEY & Lardner:

STREET: 3000 K Street, N.W., Suite 500
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Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 24104
LENGTH: 477
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                                                                                                                                                                                                                                                                                                                                                                                                Query Match 60.0%; Score 18; DB 3; Length 477; Best Local Similarity 73.1%; Pred. No. 1.1e+02; Matches 19; Conservative 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 477;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      339 AGGCTATGCGTATAGCATGATTAACC 364
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US-09-270-767-24104
Sequence 24104, Application US/09270767
; Patent No. 6703491
                                                                                                                                                                                                                                                                ; LENGTH: 477
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-8822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Drosophila melanogaster US-09-270-767-24104
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ZIP: 20007-5109
COMPUTER READABLE FORM:
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CITY: Washington
STATE: D.C.
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Best Local Similarity
Matches 19; Consern
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
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                                                               Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2108 GGCTGCGCGCAGGCATCATCAT 2133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Search completed: January 8, 2006, 17:08:34 Job time : 103 secs
                                                        SOFTWARE: Patentin Release #1.0, Ve.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/753,247
FILING DATE: 22-NOV-1996
CLASSIFICATION ATA:
APPLICATION DATA:
APPLICATION NUMBER: AT 1928/95
FILING DATE: 24-NOV-1995
ATORNEY AGENT INFORMATION:
NAME: BENT, STEEPEN A.
RESISTRATION NUMBER: 29,768
RESISTRATION NUMBER: 29,768
RESISTRATION NUMBER: 29,768
RESISTRATION NUMBER: 40433/149
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 GGCUACGCGTAGAGCAUCATGATCCU 28
                                                                                                                                                                                                                                                                                                          40433/149
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 904136
INFORMATION FOR ESO ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 2142 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 69.2
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
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LOCATION:
FEATURE:
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; LOCATION:
US-08-753-247-8
                                                                                                                                                                                                                                                                                                                                                                          TELEFAX:
TELEX: 9
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APPLICANT: PIECTAB, NIBELAUL
APPLICANT: PIECTAB, AIRE
APPLICANT: Holdin, Carl-Henrik
APPLICANT: Holdin, Carl-Henrik
APPLICANT: Holdin, Carl-Henrik
APPLICANT: Holdin, Kristofer
TITLE OF INVENTION: LIGANDS TO PDGF
FILE REFERENCE: NEX90
CURRENT APPLICATION NUMBER: US/09/859,724
CURRENT PILING DATE: 2000-09-21
PRIOR PAPLICATION NUMBER: 08/479,725
PRIOR FILING DATE: 1995-06-07
PRIOR FILING DATE: 1995-06-07
PRIOR PELICATION NUMBER: 08/479,783
PRIOR FILING DATE: 1996-03-20
PRIOR PILING DATE: 1996-03-20
PRIOR FILING DATE: 1997-12-16
NUMBER OF SEQ ID NOS: 2
SEQ ID NO 1
LENGTH: 30
TYPE: DNA
CORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TEALINE INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: Nucleic Acid Ligand
NAME/KEY: modified base
LOCATION: (6)...(30)
OTHER INFORMATION: U at positions 6, 20 and 30 is
OTHER INFORMATION: 2.fluoro-2.deoxyuridine
NAME/KEY: modified base
LOCATION: (8)..(29)
OTHER INFORMATION: C at positions 8, 21, 28, and 29 is
OTHER INFORMATION: C - fluoro-2.deoxycytidine
NAME/KEY: modified base
LOCATION: (9)..(31)
OTHER INFORMATION: G at positions 9, 15, 17, and 31 is
OTHER INFORMATION: 2.-O-Methyl-2.deoxyguanosine
NAME/KEY: modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/09859724 Patent No. US20020034506A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-859-724-1
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Sequence 2, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 8, Appli
Sequence 8, Appli
Sequence 8, Appli
Sequence 1110, A
Sequence 16217, A
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Sequence 34193, A
Sequence 145955,
Sequence 24608, A
Sequence 1, Appli
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Sequence 139288,
Sequence 29066, A
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Sequence 4, Appli
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                                                                                                                                                 January 8, 2006, 15:50:54; Search time 560 Seconds (without alignments) 443.002 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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/ cgn2 6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
/ cgn2 6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
/ cgn2 6/ptodata/1/pubpna/USO9B_PUBCOMB.seq:*
/ cgn2 6/ptodata/1/pubpna/USIOA_PUBCOMB.seq:*
/ cgn2 6/ptodata/1/pubpna/USIOB_PUBCOMB.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19587084
GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
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| 30 8 US-10-791-367-1
| 30 9 US-10-26-806-21
| 31 5 US-10-021-330-3
| 31 8 US-10-021-330-3
| 29 8 US-10-829-504A-8
| 7 29 9 US-10-813-85-8
| 7 29 9 US-10-90-21-8
| 8 US-10-90-21-8
| 4992 | 0 US-10-90-13-16217
| 4992 | 0 US-11-097-143-16216
| 493 | 0 US-10-97-143-16216
| 493 | 0 US-10-767-10-29066
| 663 | 0 US-10-767-10-29066
| 3 734 | 8 US-10-762-107-27
| 3 1359 | 0 US-10-762-107-27
| 3 3 256646 | 7 US-10-425-115-145955
| 3 3 256646 | 7 US-10-425-115-145955
| 3 3 2 2 2 3 4 US-10-425-113-14608
| 3 2 2 3 4 US-10-425-113-14608
| 4 US-10-425-113-14608
| 4 US-10-425-113-14608
| 5 US-10-425-113-14608
| 6 US-10-425-113-14608
| 7 US-10-424-599-92411
| 7 1617 | 8 US-10-421-113-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  9793542 segs, 4134689005 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Published_Applications_NA_Main:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                   OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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seq length: 200000000
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Match Length
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Perfect score:
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Maximum DB
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19
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74656, A	4, Appli	1, Appli	1, Appli	2030, Ap	2030, Ap	 Appli 	3107, Ap	1390, Ap	86, Appl	31340, A	13, Appl	12, Appl	150217,	2640, Ap	2284, Ap	422787,	319063,	319063,	662266,	788924,	847051,
Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
US-10-437-963-74656	US-10-308-936-4	US-10-308-936-1	US-10-419-256-1	US-09-938-842A-2030	US-09-938-842A-2030	US-10-087-192-1	US-10-021-323-3107	US-10-021-323-1390	US-10-767-795-86	US-10-437-963-31340	US-10-661-398-13	US-10-661-398-12	US-10-425-115-150217	US-09-922-293-2640	US-10-653-047-2284	US-09-925-065A-422787	US-10-027-632-319063	US-10-027-632-319063	US-09-925-065A-662266	US-09-925-065A-788924	US-09-925-065A-847051
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1857	1920	1932	1932	6889	6889	40633	573	652	1430	1944	12195	16061	147	353	485	602	646	646	541	602	602
52.7	52.7	62.7	62.7	62.7	62.7	52.7	62.0	62.0	52.0	52.0	62.0	52.0	61.3	61.3	61.3	61.3	61.3	61.3	0.09	0.09	60.0
18.8	18.8	18.8	18.8	18.8	18.8	18.8	18.6	18.6	18.6	18.6	18.6	18.6	18.4	18.4	18.4	18.4	18.4	18.4	18	18 (18
24	25	56	27	28	53	30	31	32	33	34	32	36	37	38	33	40	41	42	43	44	45
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ALIGNMENTS

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TYPE: DNA ORGANISM: Artificial Sequence
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27; Conservative
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Best Local Similarity
                                                                            FEATURE:
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                OTHER INFORMATION: A at position 22 is 2'-O-Methyl-2'-deoxyadenosine NAME/KEY: modified base LOCATION: (1)..(30) OTHER INFORMATION: The residues at positions 9 and 10 are connected by a hexaethylen OTHER INFORMATION: phosphoramidite linker. The residues at positions 21 and 22 are OTHER INFORMATION: connected by a hexaethylene glycol phosphoramidite linker.
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APPLICANT: Heldin, Carl-Henrik

APPLICANT: Heldin, Carl-Henrik

APPLICANT: Rubin, Krierofer

ITILE OF INVENTION: METHOD FOR TREATMENT OF TUMORS USING NUCLEIC ACID

ITILE OF INVENTION: LIGANDS TO PDGF

FILE REFERENCE: NEX90

CURRENT PILING DATE: 2004-03-02

PRIOR APPLICATION NUMBER: US/10/791,367

CURRENT FILING DATE: 2001-09-21

PRIOR APPLICATION NUMBER: 08/479,725

PRIOR PLILNG DATE: 1995-06-07

PRIOR PILING DATE: 1995-06-07

PRIOR FILING DATE: 1995-06-07

PRIOR FILING DATE: 1995-06-07

PRIOR FILING DATE: 1996-03-20

PRIOR FILING DATE: 1996-03-20

PRIOR FILING DATE: 1996-03-20

PRIOR PLILNG DATE: 1996-03-20

PRIOR PLILNG DATE: 1997-06-07
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OTHER INFORMATION: Nucleic Acid Ligand
                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                      LOCATION: (32)
OTHER INFORMATION: (3'-3'-11nked)
US-09-859-724-1
                                                                                                                                                                                                                                                                                                                                    Query Match
100.0%; Score 30; DB 3; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.00046;
Matches 30; Conservative 0; Mismatches 0; Indels
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LOCATION: (9)..(31)
OTHER INFORMATION: G at positions 9, 15, 17, and 31 is
OTHER INFORMATION: 2'-O-Methyl-2'-deoxyguanosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and 29 is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY: modified base
LOCATION: (8). (29)
LOCATION: 2, (29)
OTHER INFORMATION: C at positions 8, 21, 28, 8
OTHER INFORMATION: 2'-fluoro-2'-deoxycytidine
                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CAGGCUACGCGTAGAGCAUCATGATCCUGT 30
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Publication No. US20040224335A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Pietras, Kristian
APPLICANT: Ostman, Arne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LOCATION: (22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-791-367-1
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| Sequence 21, Application US/10926806
| Publication No. US2005096257A1
| GENERAL INFORMATION:
| APPLICANT: SHIMA, DAVID
| APPLICANT: SHIMA, DAVID
| TILLE OF INVENTION: COMBINATION THERAPY FOR THE TREATMENT OF OCULAR
| TILLE OF INVENTION: COMBINATION THERAPY FOR THE TREATMENT OF OCULAR
| TILLE REFERENCE: 112089.184 EVE-013
| CURRENT APPLICATION NUMBER: 05/56,806
| CURRENT FILING DATE: 2004-08-26
| PRIOR FILING DATE: 2004-08-26
| PRIOR FILING DATE: 2004-03-26
| PRIOR FILING DATE: 2003-08-27
| NUMBER OF SEQ ID NOS: 22
| SOFTWARE: Patentin Ver. 3.2
| SOFTWARE: Patentin Ver. 3.2
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US-10-021-330-3

Sequence 3, Application US/10021330

Publication No. US20020197617A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Aptamers as Reagents for high Throughput Screening
FILE REPERBENCE NEX78

FILE REPERBENCE NEX78

CURRENT APPLICATION UNMBER: US/10/021,330

CURRENT FILING DATE: 2001-12-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                       Gapa
NAME/KEY: modified_base
LOCATION: (22)
OTHER INFORMATION: A at position 22 is 2'-O-Methyl-2'-deoxyadenosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PEATURE:
) OTHER INFORMATION: Description of Artificial Sequence: Synthetic
) OTHER INFORMATION: anti-PDGF aptamer
US-10-926-806-21
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                                                                                                                                                                                                                                                                                                                                                         Length 30;
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100.0%; Score 30; DB 8; I
Best Local Similarity 100.0%; Pred. No. 0.00046;
Matches 30; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 30; DB 9; 90.0%; Pred. No. 0.00046; ive 3; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CAGGCUACGCGTAGAGCAUCATGATCCUGT 30
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US-10-829-504A-8
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US-10-746-565-3

Sequence 3, Application US/10746565

Publication Wo. US20050048521A1

GENERAL INFORMATION:
APPLICANT: Janjic, Nebojsa
APPLICANT: Gold, Larry
ITLE OF INVENTION: Aptamers as Reagents for high Throughput Screening
FILE REFERENCE: NEX78
CURRENT APPLICATION NUMBER: US/10/746,565
CURRENT FILING DATE: 2003-12-24
PRIOR PILING DATE: 2001-12-10
PRIOR PILING DATE: 1999-02-09
NUMBER: OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
LENGTH: 31

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OTHER INFORMATION: ligand
FEATURE:
NAME/KEY:
MAME/KEY:
MANDIACEY:
MANDIACEX:
MANDIACEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
NAME/KEY: modified base
LOCATION: (1). (31)
OTHER INFORMATION: The tat position 1 is 2'-NH2. The u's and c's at OTHER INFORMATION: positions 7, 9, 20, 21, 27, 28 and 29 are 2'-F.
OTHER INFORMATION: The a's and g's at positions 10, 15, 17, 22 and 30 OTHER INFORMATION: are 2'-O-methyl.

LOCATION: (1). (31)
OTHER INFORMATION: The g at position 10 and the a at position 22 have OTHER INFORMATION: been modified with polyethylene glycol of 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Description of Artificial Sequence: Nucleic acid OTHER INFORMATION: ligand
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100.0%; Score 30; DB 5; Length 31;
Best Local Similarity 100.0%; Pred. No. 0.00046;
Matches 30; Conservative 0; Mismatches 0; Indels
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PRIOR APPLICATION NUMBER: US/09/246,461
PRIOR FILING DATE: 1999-02-09
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Artificial Seguence
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APPLICANT: Diener, John L.
APPLICANT: Wilson, Charles
APPLICANT: Wilson, Charles
APPLICANT: McCauley, Thomas
APPLICANT: DeSouza, Errol
TITLE OF INVENTION: Stabilized Aptamers to Platelet Derived Growth Factor and Their
FILE OF INVENTION: Use as Oncology Therapeutics
FILE REFERENCE: 23239-558A
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CURRENT FILING DATE: 2004-01-21

PRIOR APPLICATION NUMBER: 10/762915

PRIOR PELLING DATE: 2004-01-21

PRIOR FILING DATE: 2004-01-21

PRIOR FILING DATE: 2003-01-21

PRIOR PELLING DATE: 2003-04-15

PRIOR PELLING DATE: 2003-04-15

PRIOR PELLING DATE: 2003-04-15

PRIOR PELLING DATE: 2003-04-21

PRIOR PELLING DATE: 2003-04-21

PRIOR PELLING DATE: 2003-04-23

PRIOR PELLING DATE: 2003-04-23

PRIOR PELLING DATE: 2003-04-23

PRIOR PELLING DATE: 2003-05-08

PRIOR PELLING DATE: 2003-05-08

PRIOR PELLING DATE: 2003-05-08

PRIOR PELLING DATE: 2003-05-08

PRIOR PELLING DATE: 2003-05-09

PRIOR PELLING DATE: 2003-01-01-06

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    Length 31;
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Query Match
100.0%; Score 30; DB 8; I
Best Local Similarity 100.0%; Pred. No. 0.00046;
Matches 30; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 29; DB 8;
Pred. No. 0.0014;
3; Mismatches C
                                                                                                                                                              1 CAGGCUACGCGTAGAGCAUCATGATCCUGT 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 8, Application US/10829504A Publication No. US20040253679A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 8, Application US/10873853; Publication No. US20050124565A1; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Epstein, David
APPLICANT: Grate, Dilara
APPLICANT: Stanton, Martin
APPLICANT: Diener, John L.
APPLICANT: Wilson, Charles
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Best Local Similarity
Matches 26; Conserva
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TITLE OF INVENTALY.

TITLE OF INVENTALIA.

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT APPLICATION NUMBER: 0/191,078

PRIOR PILING DATE: 2000-03-21

PRIOR PILING DATE: 2000-05-23

PRIOR PILING DATE: 2000-05-24

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-05-66

PRIOR PILING DATE: 2000-09-06

PRIOR PILING DATE: 2000-09-09

PRIOR PILING DATE: 2000-10-23

PRIOR PILING DATE: 2000-11-27

PRIOR PILING DATE: 2000-10-2-22

PRIOR PILING DATE: 2001-02-09

PRIOR PILING DATE: 2001-02-09

PRIOR PILING DATE: 2001-02-16
      Gaps
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89.7%; Pred. No. 0.0014;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
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Carr, Grant
Yamamoto, Robert
Forsyth, R.
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COTHER INFORMATION: aptamer
US-10-980-211-8
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Zyskind, Judith
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Trawick, Joh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 26; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Artificial
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APPLICANT:
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APPLICANT:
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APPLICANT: Grate, Dilara
APPLICANT: Grate, Dilara
APPLICANT: Stanton, Martin
APPLICANT: Diener, John
APPLICANT: Diener, John
APPLICANT: Wilson, Charles
APPLICANT: Wilson, Charles
APPLICANT: Modera, Charles
APPLICANT: DeSouza, Errol
TITLE OF INVENTION: Stabilized Aptamers to Platelet Derived Growth Factor and Their
TITLE OF INVENTION: Use as Oncology Therapeutics
CURRENT APPLICATION NUMBER: 10/129504
PRIOR APPLICATION NUMBER: 10/762915
PRIOR APPLICATION NUMBER: 10/762915
PRIOR FILING DATE: 2003-01-21
PRIOR PILING DATE: 2003-01-21
PRIOR PILING DATE: 2003-01-21
PRIOR PILING DATE: 2003-04-23
PRIOR PILING DATE: 2003-04-21
PRIOR PILING DATE: 2003-04-23
PRIOR FILING DATE: 2003-04-23
PRIOR FILING DATE: 2003-04-23
PRIOR FILING DATE: 2003-04-23
PRIOR PILING DATE: 2003-04-23
PRIOR APPLICATION NUMBER: 60/512011
PRIOR PILING DATE: 2003-04-23
PRIOR APPLICATION NUMBER: 60/512011
PRIOR PILING DATE: 2003-04-23
PRIOR APPLICATION NUMBER: 60/512011
PRIOR PILING DATE: 2003-04-23
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APPLICANT: Wilson, Charles
TITLE OF INVENTION: Stabilized Aptamers to Platelet Derived Growth Factor and Their
TITLE OF INVENTION: Use as Oncology Therapeutics
FILE REFERENCE: 2339-558A CIP2
CURRENT APPLICATION NUMBER: US/10/980,211
CURRENT PILING DATE: 2004-01-02
PRIOR APPLICATION NUMBER: 10/873853
PRIOR APPLICATION NUMBER: 10/829504
PRIOR FILING DATE: 2004-04-21
PRIOR FILING DATE: 2004-04-21
PRIOR FILING DATE: 2004-01-21
PRIOR FILING DATE: 2004-01-21
PRIOR FILING DATE: 2003-11-21
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Publication No. US20050159351A1
GENERAL INFORMATION:
APPLICANT: Grate, Dilara
APPLICANT: Diener, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: aptamer US-10-873-853-8
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δ 셤 DROSOPHILA GENES.

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RESULT 13
US-10-425-115-139288
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Publication No. US20050208558A1

GENERAL INFORMATION:

APPLICANT: Venter, J. Craig

APPLICANT: Venter, J. Craig

APPLICANT: et al.

ITILE OF INVENTION: DETECTING EXPRESSION OF 10,000 OR MORE

ITILE OF INVENTION: DROSOPHILA GENES.

TITLE OF INVENTION: DROSOPHILA GENES.

TITLE OF INVENTION: DROSOPHILA GENES.

CURRENT APPLICATION UNMBER: US/11/097,143

CURRENT PILING DATE: 1999-10-19

PRIOR FILING DATE: 1999-11-12

PRIOR FILING DATE: 1999-11-12

PRIOR FILING DATE: 1999-12-28

PRIOR FILING DATE: 1999-11-12

PRIOR FILING DATE: 1999-12-28

PRIOR FILING DATE: 1999-12-28

PRIOR FILING DATE: 1999-12-28

PRIOR FILING DATE: 1999-12-28

PRIOR FILING DATE: 1999-13-38

PRIOR FILING DATE: 1999-13-4

PRIOR FILING DATE: 2000-02-24

PRIOR PRILING DATE: 2000-03-33

NUMBER OF SEQ ID NOS: 43008

SOFTWARE: FRANCE WINDOWS Version 4.0
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APPLICANT: Venter, J. Craig
APPLICANT: et al.
TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 41310
LENGTH: 2862
TYPE: DNA
CRAMISM: Vibric cholerae
US-10-282-122A-41310
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                                                                                                                                                                                                                               Query Match 66.0%; Score 19.8; DB 7; Length 2862; Best Local Similarity 87.0%; Pred. No. 54; Matches 20; Conservative 1; Mismatches 2; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 10;
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84.6%; Pred. No. 66;
tive 0; Mismatches
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; Sequence 16216, Application US/11097143
; Publication No. US20050208558A1
                                                                                                                                                                                                                                                                                                                                                                       98 ACGCGTACAGCATCATGATCCCG 120
                                                                                                                                                                                                                                                                                                                                     7 ACGCGTAGAGCAUCATGATCCUG 29
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Best Local Similarity 84.61
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: DNA; ORGANISM: DROSOPHILA
US-11-097-143-16217
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Sequence 17734, Application US/10425115
Sequence 17734, Application US/10425115
Sequence 17734, Application US/10425115
Sequence 17734, Application US/10425115
Senemal INDEMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: APPLICANT: Apoly Thus
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21 (53222)
FILE REFERENCE: 38-21 (53222)
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 17734
LENGTH: 403
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US-10-425-115-17734
THILE REPERENCE: CLOOO'28

CURRENT APPLICATION NUMBER: US/11/097,143

CURRENT FILING DATE: 2005-04-04

PRIOR PILING DATE: 1999-10-05

PRIOR PILING DATE: 1999-10-19

PRIOR PILING DATE: 1999-10-19

PRIOR PILING DATE: 1999-10-19

PRIOR PILING DATE: 1999-10-28

PRIOR PILING DATE: 1999-10-28

PRIOR PILING DATE: 1999-10-28

PRIOR PILING DATE: 1999-11-12

PRIOR PILING DATE: 1999-11-12

PRIOR PILING DATE: 1999-11-28

PRIOR PILING DATE: 1999-11-28

PRIOR PILING DATE: 1999-11-28

PRIOR PILING DATE: 2000-01-12

PRIOR PILING DATE: 2000-01-13

NUMBER OF SEQ ID NOS: 43008

SOFTWARE: PASSEE FOR WINGOWS VERSION 4.0

SED ID NO 16216
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Matches 22; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: DROSOPHILA
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ORGANISM: Zea mays
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Gaps

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63.3%; Score 19; DB 8; Length 663; ilarity 74.1%; Pred. No. 1.1e+02; Conservative 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Micromonospora sp. strain 046-EC011
                    CURRENT FILING DATE: 2004-01-20
PRIOR APPLICATION NUMBER: USSN 60/441,126
PRIOR FILING DATE: 2003-01-21
PRIOR PILING DATE: 2003-01-21
PRIOR APPLICATION NUMBER: USSN 60/492,997
PRIOR FILING DATE: 2003-08-07
PRIOR FILING DATE: 2003-11-10
NUMBER OF SEQ ID NOS: 89
SOFTWARE: Patentin version 3.0
LENGTH: 663
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       CURRENT APPLICATION NUMBER: US/10/762,107
                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 20; Conserve
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APPLICANT: Farnet, Chris
APPLICANT: Farnet, Chris
APPLICANT: Parnet, Chris
APPLICANT: Zazopoulos, James
APPLICANT: Bachmann, Brian
APPLICANT: Bachmann, Brian
APPLICANT: Piraee, Mahmood
TITLE OF INVENTION: FARNESYL DIBENZODIAZEPINONE, PROCESSES FOR ITS PRODUCTION AND ITS
FILE REPERENCE: 3005-5US
GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Sovalic, David K.

APPLICANT: Show Yihua

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants

FILE REPERBNCE: 38-21(5322)8

CURRENT APPLICATION NUMBER: US/10/425,115

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 132288

LENGTH: 1335
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; Sequence 29066, Application US/10767701
; Sequence 29066, Application No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(5353)8
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 29066
; LENGTH: 466
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64.0%; Score 19.2; DB 7;
Best Local Similarity 83.3%; Pred. No. 83;
Matches 20; Conservative 1; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 19.4; DB 8;
Pred. No. 76;
2; Mismatches 6;
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US-10-425-115-139288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              117 CAGACAACGCGTCGAGGATTATGATGCTG 145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ) OTHER INFORMATION: Clone ID: 8548521
US-10-767-701-29066
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Publication No. US20050043297A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 72.4%;
Matches 21; Conservative
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                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Zea mays
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US-10-767-701-29066
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US-10-762-107-27/c
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US-11-121-086-38/c
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RESULT 1
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Sequence 13, Appl
Sequence 13, Appl
Sequence 456, App
Sequence 13352, A
Sequence 103, App
Sequence 749, App
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Sequence 25891, A
Sequence 25891, A
Sequence 68, Appl
Sequence 53338, A
Sequence 53338, A
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                                                                                                                                                January 8, 2006, 15:55:54 ; Search time 243 Seconds (without alignments) 89.992 Million cell updates/sec
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1: /cgn2_6/ptodata2/pubpna/USO8_NEW PUB.seq:*
2: /cgn2_6/ptodata2/2/pubpna/USO8_NEW_PUB.seq:*
3: /cgn2_6/ptodata2/2/pubpna/USO7_NEW_PUB.seq:*
4: /cgn2_6/ptodata2/2/pubpna/NET_NEW_PUB.seq:*
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6: /cgn2_6/ptodata2/2/pubpna/USO1_NEW_PUB.seq:*
7: /cgn2_6/ptodata2/2/pubpna/USO1_NEW_PUB.seq:*
8: /cgn2_6/ptodata2/2/pubpna/USO1_NEW_PUB.seq:*
9: /cgn2_6/ptodata2/2/pubpna/USO1_NEW_PUB.seq:*
9: /cgn2_6/ptodata2/2/pubpna/USO1_NEW_PUB.seq:*
10: /cgn2_6/ptodata2/2/pubpna/USO1_NEW_PUB.seq:*
                    GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
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US-10-750-185-25891

US-10-750-623-5891

US-11-121-086-68

US-10-750-185-5338

US-10-750-623-5338

US-10-750-623-26283

US-10-750-623-26283

US-10-750-623-26283

US-10-750-623-26283

US-10-750-623-26283

US-10-750-623-26283

US-10-136-527-246

US-10-995-561-11837

US-10-995-561-11837

US-10-995-561-61360

US-10-995-561-61360
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Maximum Match 100%
Listing first 45 summaries
                                                                                                       nucleic search, using sw model
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seq length: 200000000
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59.3 1110
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Match Length
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56.7
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Perfect score:
Sequence:
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47478, A
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29873, A
39532, A
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Publication No. US2005026645941
GENERAL INFORMATION:
APPLICANT: POULSEN, KIRSTEN V.
TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
FILE REFERENCE: 09138.6000-00000
CURRENT APPLICATION NUMBER: US/11/121,086
CURRENT FILING DATE: 2005-05-04
PRIOR FILING DATE: 2004-05-04
PRIOR FILING DATE: 2004-05-04
NUMBER: OF SEQ ID NOS: 107
SEQ ID NO 38 atentin version 3.3
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US-10-750-185-25891

Sequence 25891, Application US/10750185

Sequence 25891, Application US/10750185

Publication No. US20050260603A1

GENERAL INFORMATION:

APPLICANT: MAI GENOMICS, INC.

APPLICANT: ROSENFELD, David

APPLICANT: ROSENFELD, David

APPLICANT: PATIN, Dennis

TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS

FILE REFERENCE: MM1100-2

CURRENT APPLICATION HUMBER: US/10/750,185

CURRENT FILING DATE: 2003-12-31
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US-10-467-657-2601

US-11-108-80-817-10-80-91

US-10-947-249-82

US-11-121-086-91

US-11-000-688-971

US-10-93-025-23

US-10-750-623-57644

US-10-750-623-57644

US-11-136-527-2256

US-10-85-134-788

US-10-750-185-29873

US-10-750-185-29873

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; ORGANISM: Homo sapiens
US-11-121-086-38
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GURLEALL INFORMATION:
GRAPALICANT: INFORMATION:
APPLICANT: MAINTON:
APPLICANT: MAINTON
APPLICANT: ACSENFER, Richard
APPLICANT: ACSENFER, Bichard
APPLICANT: ACSENFER, Bichard
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
FILE REFERENCE: MAILON-100-1
CURRENT APPLICATION NUMBER: US/10/750,623
CURRENT FILING DATE: 2003-12-31
CURRENT FILING DATE: 2003-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PALENTIN VERSION 3.1
SEQ ID NO 53338
LENGTH: 762
                                                59.3%; Score 17.8; DB 7; Length 146656; 65.5%; Pred. No. 1.4e+02; ive 3; Mismatches 7; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: MINIMATION.
APPLICANT: MINIMATION.
APPLICANT: MINIMATION.
APPLICANT: MINIMATE SOURCE.
APPLICANT: ROSENFELD, David
APPLICANT: ROSENFELD, David
APPLICANT: BATES, Stephen
APPLICANT: BATES, Stephen
APPLICANT: BATES, Stephen
APPLICANT: BATES, STEPHEN
TITLE REFERENCE: MINIMATION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MINIMATER: US/10/750,185
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR PRILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PALENT VERSION 3.1
SEQ ID NO 5338
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66.7%; Pred. No. 94;
tive 3; Mismatches
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... Sequence 53338, Application US/10750185
... Publication No. US20050260603A1
... GENERAL INFORMATION:
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Publication No. US20050287531A1
GENERAL INFORMATION:
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ORGANISM: Bovine 19866881728240
                                                     Query Match 59.3
Best Local Similarity 65.5
Matches 19; Conservative
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Matches 18; Conserv
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     US-11-121-086-68
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Publication No. US2050266459A1

GENERAL INCOMPATION:
APPLICANT: POULSEN, TIM S.
TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
FILE REFERENCE: 09138.600-00000
CURRENT APPLICATION NUMBER: US/11/121,086
CURRENT APPLICATION NUMBER: 05/57,570
PRIOR APPLICATION NUMBER: 60/567,570
PRIOR PILING DATE: 2004-05-04
NUMBER OF SEQ ID NOS: 107
SOFTWARE: Patentin version 3.3
SEQ ID NO 68
LENGTH: 146656
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APPLICANT: BATES, Stephen
APPLICANT: BATES, Stephen
APPLICANT: PANTIN Dennis
TITLE OF INVENTION: METHODS AND SYSTEMS FOR INPERRING BOVINE TRAITS
FILE REPRESENCE: MM11100-1
CURRENT APPLICATION NUMBER: US/10/750,623
CURRENT FILING DATE: 2003-12-31
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Best Local Similarity 65.5%; Pred. No. 65;
Matches 19; Conservative 3; Mismatches
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; Sequence 25891, Application US/10750623
; Sequence 25891, Application US/10750623
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DeNISE, Suc K.
; APPLICANT: ROSENFELD, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/437,482 PRIOR FILING DATE: 2002-12-31
          60/437,482
                                                                                                                                                                            ; ORGANISM: Bovine 19866881126825
US-10-750-185-25891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , ORGANISM: Bovine 19866881126825
US-10-750-623-25891
PRIOR APPLICATION NUMBER: US 60/.
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SEQ ID NO 25891
LENGTH: 1110
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SOFTWARE: PatentIN version 3.1
SEQ ID NO 25891
LENGTH: 1110
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ORGANISM: Homo sapiens
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APPLICANT: MINISTER, RICHARD
APPLICANT: MINISTER, RICHARD
APPLICANT: MOSSINEEL, Sue K.
APPLICANT: MOSSINEEL, David
APPLICANT: MOSSINEEL, David
APPLICANT: HOLM, Tom
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: BATIN, Demnis
TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MOTION-1
CURRENT APPLICATION NUMBER: US/10/750,623
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PALENTIN Version 3.1
SEQ ID NO 26283
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APPLICANT: Wyeth
APPLICANT: Mounts, William M
APPLICANT: Mounts, William M
TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
FILE REFERENCE: 031896-041000 (AM101086)
CURRENT APPLICATION NUMBER: US/11/136,527
CURRENT APPLICATION NUMBER: US 60/574,294
PRIOR APPLICATION NUMBER: US 60/574,294
PRIOR PILING DATE: 2005-05-26
NUMBER OF SEQ ID NOS: 362830
SOFTWARE: Patentin version 3.2
SEQ ID NO 4382
LENGTH: 1400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 57.3%; Score 17.2; DB 7; Length 1400; Best Local Similarity 63.3%; Pred. No. 1.3e+02; Matches 19; Conservative 3; Mismatches 8; Indels 0;
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                                                                                                                                                               Sequence 26283, Application US/10750623
Publication No. US20050287531A1
GENERAL INFORMATION:
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US-11-136-527-224/c
; Sequence 224, Application US/11136527
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-4382
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Best Local Similarity 70.41
Matches 19; Conservative
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US-11-136-527-4382/c
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APPLICANT: Hoffmann, Marcel
APPLICANT: Spittaels, Koenraad F. F.
APPLICANT: Spittaels, Koenraad F. F.
APPLICANT: Laenen, Wendy
TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
TITLE OF INVENTION: Amyloid-Beta Protein Production
FILE REFERENCE: P27,800-B USA
CURRENT APPLICATION NUMBER: 80/11/127,877
CURRENT FILING DATE: 2005-05-12
PRIOR PLING DATE: 2004-05-12
PRIOR PLING DATE: 2004-05-12
PRIOR PLING DATE: 2004-08-24
NUMBER OF SEQ ID NOS: 590
SOFTWARE: Patentin version 3.3
SEQ ID NO 20
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APPLICANT: BATES, Stephen
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMI1100-2
GURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
FRIOR PLICE OF SEQ ID NOS: 64922
SOFTWARE: Patentin version 3.1
SEQ ID NOS: 62283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58.0%; Score 17.4; DB 7; Length 1002; 66.7%; Pred. No. 98; tive 3; Mismatches 6; Indels 0;
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                             6; Indels
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Best Local Similarity 66.7%; Pred. No. 94; Matches 18; Conservative 3; Mismatches
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                                                                                                      123 GGCTACTCGGAGTGCATCGTGACCGTG 97
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Publication No. US20050260603A1
GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: DeMISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
                                                                                                                                                                                                                                  Sequence 20, Application US/11127877; Publication No. US20050287565A1; GENERAL INFORMATION:
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; ORGANISM: Bovine 19866881128530
US-10-750-185-26283
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Best Local Similarity 70.41
Matches 19; Conservative
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Matches 18; Conservative
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; ORGANISM: Homo sapiens
US-11-127-877-20
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US-10-750-185-26283
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-11799
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Publication No. US20050272054A1

GENERAL INFORMATION

APPLICANT: CARGILL, Michele et al.

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF

TITLE OF INVENTION: DETECTION AND USES THEREOF

TITLE OF INVENTION: DETECTION AND USES THEREOF

FILE REFERENCE: CLO01559

CURRENT APPLICATION NUMBER: US/10/995,561

CURRENT PILING DATE: 2004-11-24

NUMBER OF SEQ ID NOS: 85702

SSOCIATE REFERENCE: CLO04-11-24

NUMBER OF SEQ ID NOS: 85702

SSOCIATE REFERENCE: Andows Version 4.0

SEQ ID NO 11799
Publication No. US20050287570A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Wyearth William M
TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes FILE REPERENCE: 011896-041000 (AM101086)
CURRENT APPLICATION: NUMBER: US/11/136,527
CURRENT FILING DATE: 2005-05-25
PRIOR PAPLICATION NUMBER: US 60/574,294
PRIOR APPLICATION NUMBER: US 60/574,294
PRIOR PILING DATE: 2005-05-26
NUMBER OF SEQ ID NOS: 362830
SOFTWARE: Patentin version 3.2
SEQ ID NO 224
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Sequence 286, Application US/11136527

Sequence 286, Application US/11136527

Sequence 286, Application US/11136527

Sequence 286, Application US/11136527

GENERAL INFORMATION:

APPLICANT: Wyeth

TILLE OF INVENTION:

FILE REPERENCE: 031896-041000 (AM101086)

CURRENT APPLICATION NUMBER: US/11/136,527

CURRENT FILING DATE: 2005-05-25

PRIOR FILING DATE: 2005-05-26
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Pred. No. 1.3e+02;
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57.3%; Score 17.2; DB 7;
Best Local Similarity 63.3%; Pred. No. 1.5e+02;
Matches 19; Conservative 3; Mismatches 8;
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SOFTWARE: PatentIn version 3.2
SEQ ID NO 286
LENGTH: 4347
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Best Local Similarity 66.7%;
Matches 20; Conservative
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US-11-136-527-286
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US-11-136-527-224
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US-10-995-561-11799/c
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Publication No. US20050272054A1

Publication No. US20050272054A1

GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
TITLE OF INVENTION: UNMBER: US/10/995,561
CURRENT APPLICATION UNMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FRESEQ for Windows Version 4.0
SEQ ID NO 11837
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TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CL001559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT APPLICATION NUMBER: US/10/995,561
SOFTWARE: FREUSEQ for Windows Version 4.0
SEQ ID NO 51360
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Length 201
56.7%; Score 17; DB 6; Length 201
72.0%; Pred. No. 1.2e+02;
tive 2; Mismatches 5; IndelB
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Best Local Similarity 72.0%; Pred. No. 1.2e+02;
Matches 18; Conservative 2; Mismatches 5; Indels
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                                                                                                          1 CAGGCUACGCGTAGAGCAUCATGAT 25
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; Publication No. US20050272054A1
; GENERAL INFORMATION:
  Query Match
Best Local Similarity 72.0
Matches 18; Conservative
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CORGANISM: Homo sapiens
US-10-995-561-61360
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CORGANISM: Homo sapiens
US-10-995-561-11837
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US-10-995-561-61360/c
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US-10-995-561-11837/c
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Run on:

Sequence:

Minimum DB Maximum DB

Database

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AY058696 Drosophil
CQ588459 Sequence
AY052083 Drosophil
CQ588459 Sequence
AC101990 Drosophil
AC101373 Homo sapi
AC10879 Homo sapi
AC10379 Homo sapi
AY261364 African B
AY261364 African B
AY261364 African B
AY261369 Mus muscu
AC150605 Callithri
AC11047 Mus muscu
AC150605 Callithri
AC11047 Mus muscu
AC15658 Homo sapi
AC15659 Homo sapi
AC16598 Sequence
CQ878999 Sequence
AX653922 Sequence
AX65392 Sequence
AR004312 Synechocy
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BX545849 Mouse DNA
AP003943 Oryza sat
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Patent: WO 2005020972-A 21 10-MAR-2005;
Byetech Pharmaceuticals, Inc. (US)
Location/Qualifiers
1. 30
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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AC151312 Rattus no
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Rattus norvegicus clone CH230-285A15, WORKING DRAFT SEQUENCE.
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THTG: PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
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Janjic,N. and Gold,L.
Determining non-nucleic acid molecule binding to target by competition with nucleic acid ligand
Patent: US 6670132-A 3 30-DEC-2003;
Gilead Sciences, Inc.; Foster City, CA
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/organism="unknown"
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Description of Artificial Sequence: Nucleic acid ligand CC The apposition of Artificial Sequence: Nucleic acid ligand CC The The u's and c's at positions 7, 9, 20, 21, 27, 28 and 29 are 2'-F.
C The a's and g's at positions 10, 15, 17, 22 and 30 are 2'-O-methyl.
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                                              1 (bases 1 to 30)
Pietras, K., Ostman, A., Heldin, C.-H. and Rubin, K.
Method for treatment of tumors using nucleic acid ligands to PDGF
Patent: US 6699843-A 1 02-MAR-2004;
Gilead Sciences, Inc.; Foster City, CA
Location/Qualifiers
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Sciurognathi; Murcidea; Muridae; Murinae; Rattus.

(E 1 (Dasea 1 to 214312)

(E 1 (Dasea 1 to 214312)

(E 214312)

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Rat Genome Sequencing Consortium.
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Direct Submission
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REFERENCE AUTHORS TITLE JOURNAL

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COMMENT

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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html). NOTE: This is a 'working draft' sequence. It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have
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Rattus norvegicus clone CH230-174P11, WORKING DRAFT SEQUENCE, 2
may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shocgun sequence only contigs will be indicated in the feature
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This sequence will be replaced
by the finished sequence as soon as it is available and
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1 214332: contig of 214332 bp in length.
Location/Qualifiers
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75.0%; Pred. No. 99;
ive 3; Mismatches
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clone_end:Sp6"
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clone_end:T7"
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/db xref="taxon:10116"
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/note="clone_boundary
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clone_end:Sp6
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Best Local Similarity 75.0v
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On May 13, 2003 this sequence version replaced gi:23265213. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCUS AJ616913 6002 bp DNA linear PLN 11-JUN-2004
DEFINITION Sordaria macrospora pro40 gene for putative signalling cascade
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NOTE: Bstimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a "working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Pred. No. 1.98+02;
Fred. No. 1.98+02;
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clone_end:T7"
complement(3044. .3574)
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/estimated_length=unknown
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/db_xref="taxon:10116"
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ilarity 72.4%;
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                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sclurognathi, Muroldea, Muridae, Murinae, Rattus.
                                                                                                AC123112.4 GI:30580864
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
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                                                                                                                                                 Rattus norvegicus (Norway rat)
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1 CAGGCUACGCGTAGAGCAUCATGATCCU 28

/number=2

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Query Match 66.7%; Score 20; DB 15; Length 6002; Best Local Similarity 71.4%; Pred. No. 4.3e+02; Matches 20; Conservative 3; Mismatches 5; Indels
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/product="putative signalling cascade component"
/product="putative signalling cascade component"
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/db xref="GI:39645991"
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AADKASYSKYPAPPTSSSAASASASIAPLPGLPPLPSFPLPPGASSSAAPLPYPD
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APPEDLEGGMATHLDQNSGQYYYIHLAYQATQMFFPKGPNDISHBISBHAAPLSPTASYTGND
LASPLLGGKAGLASPHFPQTPGYYYIHLAYBAABSGFTGPPPSAGVDMYKTMPTNG
VYFGPYLRYVNMDLEKGIWHGSIMIVTDAPQPPTIHIHLSVDLSPNPRQLIPHNIWTH
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VSDTKEDMMEIFHTDASGAAREYKKLMARRNYVAIVAYDPDAAVNGGMGGSMMNGQGG
GGYAASVHSGGSGGNGGGLNKLSLAVDFVVQGDGAFTATTKYGPVIVPHLEYGH"
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PSTNQNERAKLGGVGFWWKDILQKNVECGGFHVQLGLGDQIYGDRLWREVPILKQWLS
IAGRENRKNVPWTARHEEDVTHAYFHYYTSHFDQPFWREAFAQIPHVLQIDDHDIFDG
                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (09-DEC-2003) Witzel-Schloemp K., LS Allgemeine und
Molekulare Botanik, Ruhr-Universitaet Bochum, Universitaetsstrasse
150, 44780 Bochum, GERMANY
Location/Qualifiers
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ETVETLANTFATGKKAVNSTYNLLGKVTSSVAGVVGGKEVVAHGFKEVKRAVGKSGLM
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                                                                                                                                                                                    Witzel-Schloemp, K., Strauch, P., Zhang, H. and Kueck, U. Molecular genetic characterization of the developmental mutant pro40 from Sordaria macrospora: Identification of a putative component of a signaling cascade Unpublished
                                                                                                                      Bukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Sordariales; Sordariaceae; Sordaria.
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                                         pro40 gene; putative signalling cascade component.
Sordaria macrospora
Sordaria macrospora
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| /organism="Sordaria macrospora"
| /mol_type="genomic DNA"
| /strain="wild type S 48977"
| /db_xref="taxon:5147"
| 348. 4360
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|gene="pro40"
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/gene="pro40"
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/gene="pro40"
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/gene="pro40"
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Witzel-Schloemp, K.
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Continuation (11 of 41) of BX571965 from base 1000001 (BX571965 Burkholderia pseudomallei
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CP000010 23/c
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BX571965 10
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Zea mays strain B73 clone ZMMBBC0059P07, *** SEQUENCING IN PROGRESS ***, 22 unordered pieces.
AC155516
AC155516.2 GI:58082376
HTGS-PHASE1.
Zea mave
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1 (bases 1 to 17239)
Chan, A.P., Pertea, G., Zheng, L., Cheung, F., Lee, D., Koo, H., Utterback, T.R., Feldblyum, T.V., Rabinowicz, P., Fraser, C.M., Schubert, K., SanMiguel, P., Ma, J., Pontaroli, A.C., Rohlfing, T., Budiman, A., Bedell, J.A., Lakey, N., Barbazuk, B., Bennetzen, J. and Quackenbush, J.
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Submitted (25-JAN-2005) The Institute for Genomic Research (TIGR), 9712 Medical Center Dr, Rockville, MD 20850
On Jan 25, 2005 this sequence version replaced gi:57863037.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submitsed (15-JAN-2005) The Institute for Genomic Research (TIGR) 9712 Medical Center Dr, Rockville, MD 20850 3 (bases 1 to 172391)
                                                                                                                Direct Submission
Submitted (12-NOV-2004) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
On Nov 12, 2004 this sequence version replaced gi:54697207.
Draft Sequence Produced by DOE Joint Genome Institute
Submitted (28-OCT-2004) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
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Finishing Completed at Stanford Human Genome Center
www.shog.stanford.edu
Quality: Phrap Quality >=40 100% of Sequence;
Estimated Total Number of Errors is 0.
Location/Qualifiers
1. .163878
/organism="Branchiostoma floridae"
/mol_type="genomic DNA"
/db_xref="taxon:7739"
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                        Drive, Walnut Creek, CA 94598
4 (bases 1 to 163878)
Stanford Human Genome Center.
DOE Joint Genome Institute
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Branchiostoma floridae
Eukaryota, Metazoa, Chordata, Cephalochordata, Branchiostomidae,
Branchiostoma.
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3 (bases I to 163878)
Stanford Human Genome Center.
DOE Joint Genome Institute
DIEST Submission
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Branchiostoma floridae clone CH302-18L14, complete sequence.
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DOE Joint Genome Institute and Stanford Human Genome Center.

Direct Submission
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Pred. No. 5.3e+02;
2; Mismatches 5; Indels 0
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                                                                                                                      NOTE: This is a 'working draft' sequence. It currently consists of 22 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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contig of 6239 bp in length
contig of 8265 bp in length
contig of 8265 bp in length
gap of unknown length
contig of 1841 bp in length
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contig of 1841 bp in length
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g of 4571 bp in length
if unknown length
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gap of unknown length
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|mol_type="genomic DNA"
|strain="B73"
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/clone="ZMMBBC0059P07"
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AC145730 174912 bp DNA linear HTG 16-JUN-2004
Zea mays clone ZMMBBC0036A01, *** SEQUENCING IN PROGRESS ***, 2
ordered pleces.
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[Chases I to 174912]

[Birran, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N.,
Barran, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N.,
Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y.,
Collymore, A., Cook, T., Cooke, P., Corum, B., DeArellano, K.,
Collymore, A., Cook, Cooke, C., Dorris, L., Erickson, J., Farc, S.,
Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S.,
Graham, L., Grand, Pierre, N., Hafez, N., Hagopian, D., Hagos, B.,
Hall, J., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C.,
Lindblad-Toh, K., Liu, X., Lui, A., Mabbitt, R., MacLean, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD clade, Panicoideae, Andropogoneae, Zea. [ bases I to 174912]
Birren, B., Nusbaum, C., Lander, E., Butler, E., Wing, R., Bharti, A.K. and Messing, J.
Zea mays, clone ZMMBBC0036A01
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HTG; HTGS_PHASE2; HTGS_FULLTOP; HTGS_ACTIVEFIN.
Zea mays
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/estimated length=unknown 40263. .40362 /estimated length=unknown 42645. .42744 /estimated length=unknown 63101. .63200
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/estimated length-unknown 112609. .112708
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79102. .79201
/estimated length=unknown
80764. .80863
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160008. .160107
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/estimated length=unknown 69775. .69874
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TITLE JOURNAL

AUTHORS REFERENCE

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I81826 bp DNA linear HTG 25-JAN-2005 Zea mays strain B73 clone ZMMBBC0177II1, *** SEQUENCING IN PROGRESS ***, 33 unordered pieces.
consists of 2 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces of believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

1 28758 contig of 28758 bp in length 28759 28859 contig of 146054 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="CHORI-201 Maize B73 BAC EcoRI Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66.7%; Score 20; DB 14;
75.0%; Pred. No. 5.5e+02;
iive 2; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25981 AGACAACGCGTCGAGCATTATGATGCTG 26008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 AGGCUACGCGTAGAGCAUCATGATCCUG 29
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/cultivar="B73"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /estimated_length=100
                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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Best Local ?
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REFERENCE
AUTHORS
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Birren, 320 Charles Street, Cambridge, MA 02141, USA

ResearChi, 320 Charles Street, Cambridge, MA 02141, USA

Birren, B., Nusbaum, C., Lander, E., Butler, E., Wing, R., Bharti, A.K.,

Messing, J., Abouelleil, A., Allen, N., Anderson, M., Anderson, S.,

Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boguslarkiy, L.,

Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A.,

Cook, A., Cooke, P., Corum, B., DeArellano, K., Diaz, J.S., Dodge, S.,

Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P.,

FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L.,

Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J.,

Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A.,

Karatas, A., Kells, C., Landers, T., Levine, R., Jindblad-Toh, K.,

Liu, G., Liu, X., Lui, A., Mabbitt, R., MacLean, C., Macdonald, P.,

Major, J., Manning, J., Matthews, C., McCarthy, M., Meldrim, J.,

Meneus, L., Mihova, T., Matthews, C., McCarthy, M., Meldrim, J.,

Manning, J., Matthews, C., O'Connor, T., O'Donnell, P.,

O'Neil, D., Oliver, J., Peterson, K., Phukhang, P., Pierre, N.,

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Roman, J., Schauer, S., Schubback, R., Stevery, P., Smith, C.,

Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M.,

Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., V.,

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Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Birect Submission

Submitted (16-JUN-2004) Whitehead Institute/MIT Center for Genome

Research, 320 Charles Street, Cambridge, MA 0214, USA

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RW/RepeatMasker:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center project name: 129606

Center clone name: 36 A 1

This consensus in formation

This consensus is derived from a shotgun assembly that has been manually curated. It is the best representation of the BAC that we can generate without further laboratory work. The draft assembly has been edited, and if possible, ends identified by vector as well as by BAC end sequences, and contigs ordered and oriented. Bases that are not Ns are either above Q20 or manually edited. This assembly was performed with Arachne (Genome Res. 2002 12: 177-189; Genome Res. 2003 13: 91-96). All trace files for this project are available at the NCBI trace repository
Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, T., Mienga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vayman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M., Direct, Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Butler, E and Wing, R: Arizona Genomics Institute, Biological Sciences West, 448A, P.O. Box 210088, University of Arizona, Tucson, AZ 85721, USA (http://www.genome.arizona.edu)
                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (23-JUL-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bharti, AK and Messing, J: The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers, The State University of New Jersey, 190 Frelinghuysen Road, Piscataway, NJ 08854, USA
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Center: Whitehead Institute/MIT Center for Genome Research
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Contact: sequence_submissions@broad.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (http://pgir.rutgers.edu)
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TITLE JOURNAL

COMMENT

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Gaps

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5; Indels

Length 174912;

.28858

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Submitted (25-JAN-2005) The Institute for Genomic Research (TIGR), 9712 Medical Center Dr, Rockville, MD 20850 On Jan 25, 2005 this sequence version replaced gi:57863095.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (15-JAN-2005) The Institute for Genomic Research (TIGR),
9712 Medical Center Dr, Rockville, MD 20850
                                                                                                                                                                  Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
                                                                                                                                                                                                                                                                                1 (bases 1 to 181826)
Chan, A.P., Pertea, G., Zheng, L., Cheung, F., Lee, D., Koo, H.,
Chan, A.P., Pertea, G., Zheng, L., Cheung, F., Lee, D., Koo, H.,
Chubert, K., SanMiguel, P., Ma, J., Pontaroli, A.C., Rohlfing, T.,
Budiman, A., Bedell, J.A., Lakey, N., Barbazuk, B., Bennetzen, J. and
Quackenbush, J.
Consortium for Maize Genomics - BAC skim sequencing and assembly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
2. (Dasea 1 to 181826)
Chan, A.P., Pertea, G., Zheng, L., Cheung, F., Lee, D., Koo, H.,
Utterback, T.R., Feldblyum, T.V., Rabinowicz, P., Fraser, C.M.,
Utterback, T.R., SanMiguel, P., Ma, J., Pontaroli, A.C., Rohlfing, T.,
Budinan, A., Bedell, J.A., Lakey, N., Barbazuk, B., Bennetzen, J. and
Quackenbush, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chan, A.P., Pertea, G., Zheng, L., Cheung, F., Lee, D., Koo, H.,
Utterback, T.R., Feldblyum, T.V., Rabinowicz, P., Fraser, C.M.,
Schubert, K., SanMiguel, P., Ma, J., Pontaroli, A.C., Rohlfing, T.,
Budinan, A., Bedell, J.A., Lakey, N., Barbazuk, B., Bennetzen, J. and
Quackenbush, J.
AC155574.2 GI:58082433
HTG; HTGS_PHASE1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 181826)
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(http://www.ncbi.nlm.nih.gov/Traces/trace.fcgi?). An exact list of reads used in this assembly are available at http://www.broad.mit.edu/annotation/plants/maize/randomclones.html.

* NOTE: This is a 'working draft' sequence. It currently

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166837: gap of unknown length
168226: contrig of 1289 bp in length
168226: gap of unknown length
17 170510: contrig of 2284 bp in length
17 170610: gap of unknown length
181826: contrig of 11216 bp in length
10 181826: contrig of 11216 bp in length.
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58010. .158109
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 166738
166838
168127
168227
170511
                                                                                                        source
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                                                                                         FEATURES
                                                                           NOTE: This is a 'working draft' sequence. It currently consists of 33 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               f unknown length
of 4179 bp in length
f unknown length
g of 1923 bp in length
f unknown length
f unknown length
of 10536 bp in length
f unknown length
f unknown length
f unknown length
g of 3828 bp in length
f unknown length
g of 7089 bp in length
f unknown length
f unknown length
g of 1472 bp in length
f unknown length
                                                                                                                                                                                                      g of 2171 bp in length
if unknown length
of 1049 bp in length
of unknown length
g of 11347 bp in length
g of 11347 bp in length
g of 754 bp in length
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f unknown length
g of 6500 bp in length
f unknown length
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g of 6464 bp in length
f unknown length
g of 4215 bp in length
f unknown length
g of 2112 bp in length
f unknown length
                                                                                                                                                                                                                                                                                                                          of 17467 bp in length
unknown length
of 5095 bp in length
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bp in length
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of 5218 bp in length
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                          Web site: http://www.tigr.org/tdb/tgi/maize/
Contact: maize@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  bp in length
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unknown 1
of 2150 b
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of 5221 b
unknown 1
of 6885 b
unknown 1
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of 4415 h
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of 1752 b
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of 3153
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Seq_lib_id: ZGEP
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ITVLEKTLRLAHPVIPYITETIWQSVKPLVDGVEGDTIMLQALPQYDVANFNQBALDD
IEWYKAFITSTRULARAYDINGKFPLEWNLKAANBODARIENKPVLVSLAKLESIR
VLADGEATPACATALVGKSELMIPWAGLIDKDAELDRLAKEIAKTQGEIARIEGKLGN
BGFVAKAPBAVITKERKLAGYQEALVKLEQQKATIAAL"
COMPIEMENT (5205. .6182)
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PID:43302; identified by sequence similarity; putative"
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GISLKPGEGMDEMKYDMCGAASVFGTWKAIAKLGLPLNVIGVLAGCENMPGSNAYRPG
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Direct Submission
Submitted (14-JUN-2000) The Institute for Genomic Research, 9712
Medical Center Dr. Rockville, MD 20850, USA
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Heidealberg'J.F., Elsen,J.A., Nelson,W.C., Clayton,R.A., Gwinn,M.L.,
Heidealberg'J.F., Elsen,J.A., Nelson,W.C., Clayton,R.A., Gwinn,M.L.,
Gill,S.R., Haft,D.H., Hickey,E.K., Peterson,J.D., Umayam,L.,
Gill,S.R., Nelson,K.E., Read,T.D., Tettelin,H., Richardson,D.,
Ermolaeva,M.D., Vamathevan,J., Bass,S., Qin,H., Draggi,I.,
Sellers,P., McDonald,L., Utterback,T., Fleishmann,R.D.,
Nierman,W.C. and White,O.
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PID:43309 PID:537102; identified by sequence similarity;

    10205 / Organism="Vibrio cholerae Ol biovar eltor str. N16961"

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Dibrio cholerae Ol biovar eltor str. N16961
Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae; Vibrio.
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0
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75.0%; Pred. No. 5.5e+02;
tive 2; Mismatches 5; Indels 0;
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          168127. .168226
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MVDRAHLLEWHPEKSSREYQVIEALARQTFGVLLTTATPEQLGRESHFALLLDAD
RFYDYBAFVKBERGYARVADAVTALFSGEKLSDBANKITELLSBAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ASEDEIALARQELIDNIMDRHGTGRVLFRNTRAAIKGFPVRNVHLLPLEIPSGYTTSM
RVAGMIGGALPRARAMMLYPERIPOPERGESSSWQPPSRNWHLLEFFKVRAKRSEKI
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RVAGMIGGARATALOPERALEREGIRATYPHEGNSIIERDKAAYFACEGGAQOLICSE
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VTPAEHMMVPSYPGLPYEGATITFDRDTALSREDMHFISWEHPWVQGGIDLLMSEGVG
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VEFESFNRQLSPVNRHLASKLVSSVQHDVHRLITASETAVEPRVSAIREQAQRDMQQS
LNSELERLLALKAVNPNIRDEEIEVLDQQIKELTGYIAQAQYQLDSLRLIVVAHN"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /Software similar to GB:U00096 PID:1786245; identified by sequence similarity; putative"
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Gaps ó Score 19.8; DB 1; Length 10205; Pred. No. 5.5e+02; 1; Mismatches 2; Indels 0; ch 66.0%; 1 Similarity 87.0%; 20; Conservative Query Match Best Local Similarity Matches

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7 ACGCGTAGAGCAUCATGATCCUG 29

2363 Aceceracacarcardarces 2385 ઠે g Search completed: January 8, 2006, 16:24:45 Job time : 1732 secs

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January 8, 2006, 15:08:49; Search time 2518 Seconds (without alignments) 557.431 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
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                                                                           OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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30
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Perfect score:
Sequence:
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                                                                                                             Run on:
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

82156650

41078325 segs, 23393541228 residues

Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

gb_est1:; gb_est2:;; gb_htc:3:;; gb_est4:; gb_est5:;; gb_est7:; gb_gss1:; gb_gss2:; EST: * Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	BW778170 BW778170 CC786547 BL285D D0 AU170138 AU170138 BJ716634 BJ716634 BX306829 CES1821 tigr-g8s- AQ405865 HS 5043 B AJ745356 AJ745356 CC494201 CH240 329 DN711869 CLJ97-H05 DN686483 CGX47-C07 CLG40521 CH213-1NO CLG40521 CH213-1NO CLG40521 CH213-1NO CLG4051 CH213-1NO CC914756 CH13-10 E BU74556 CH13-10 E BU745540 CH18-11 E	
SUMMARIES	BW778170 CO786247 AU170138 BW3106234 BW3106829 CE251821 AAQ405865 AA7745356 CA94201 DN711869 DN711869 DN711869 DN711869 CC1640951 CC2944756 DN745549 CC1445434 BU745550 CC982446 BU745549	11 10000
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Score	00000000000000000000000000000000000000	
Result No.		٠ ر

BX558657 BX558657	CO294995 EK208126.	BX562437 BX562437	BX556173 BX556173	BX568347 BX568347	BX568861 BX568861	BX551247 BX551247	AI404024 GH23607.5	AG385831 Mus muscu	AQ181478 HS 3219 A	BH035476 RPCI-24-2	CC934167 ZMMBBc054	BJ566348 BJ566348	BU363359 603790407	AQ875939 V131C6 mT	AQ251296 T30110-Sp	CR858601 Pongo pyg	BE125931 DG1 59 G0	DR063891 ip71e04.g	BF528338 602044251	BZ335768 hz26g05.g	CW487118 fsbb001f2	BZ628162 ih58c10.b
BX558657	CO294995	BX562437	BX556173	BX568347	BX568861	BX551247	AI404024	AG385831	AQ181478	BH035476	CC934167	BJ566348	BU363359	AQ875939	AQ251296	CR858601	BE125931	DR063891	BF528338	BZ335768	CW487118	BZ628162
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65.3	65.3	65.3	65.3	65.3	65.3	65.3	65.3	65.3	64.7	64.7	64.7	64.7	64.7	64.7	64.7	64.7	64.0	64.0	64.0	64.0	64.0	64.0
19.6	19.6	19.6	19.6	19.6	19.6	19.6	19.6	19.6	19.4	19.4	19.4	19.4	19.4	19.4	19.4	19.4	19.2	19.2	19.2	19.2	19.2	19.2
c 23	c 24	c 25	c 26	c 27		29	30	c 31	c 35	33	c 34	c 35	c 36	c 37	c 38	c 39	40	c 41	42	c 43	C 44	45

ALIGNMENTS

RESULT 1	
2/0/1	
	BW778170 389 bp mRNA linear EST 10-AUG-2005
DEFINITION BW7	778170 Amphioxus Branchiostoma floridae unpublished cDNA library,
gae	gastrula whole animal Branchiostoma floridae cDNA clone bbga048003
	, mKNA sequence.
ž	
	BW778170.1 GI:66380664
So	
	Branchiostoma floridae (Florida lancelet)
ORGANISM Bra	Branchiostoma floridae
Enk	Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
	Branchiostoma.
REFERENCE 1	
SS	Yu,J., Holland,L.Z., Shin-i,T., Kohara,Y., Satou,Y. and Satoh,N.
	Expressed genes in Branchiostoma floridae
AL.	Unpublished (2005)
COMMENT	Contact: Tadasu Shin-i
Cer	Center For Genetic Resource Information
Nat	National Institute of Genetics
111	1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel:	1; 81-559-81-6856
Fax:	K: 81-559-81-6855
Ema	Email: tshini@genes.nig.ac.jp
If	If you want to have a cDNA clone for this EST or if you have any
ane	questions, please send an e-mail to Nori Satoh
28)	(satoh@ascidian.zool.kyoto-u.ac.jp) and its cc to Yutaka Satou
3	(yutaka@ascidian.zool.kyoto-u.ac.jp).
FEATURES	Location/Qualifiers
source	1389
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ORIGIN	
Query Match	
Best Local Similarity Matches 21; Conser	//.s*; vative ?

2 AGGCUACGCGTAGAGCAUCATGATCCU 28

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SDOG

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthopterygii; Percomorpha; Atherinomorpha; Acanthopterygii; Percomorpha; Atherinomorpha; Beloniformes; Addianichthyidae; Oryzinae; Oryzias.

1 (bases 1 to 724)

1 (bases 1 to 724)

1 (bases 1 to 724)

2 (bases 1 to 724)

3 (bases 1 to 724)

4 (bases 1 to 724)

5 (contact: Tadasu Sihini

Center For Genetic Resource Information

National Institute of Genetics

111 Yata, Mishima, Shizuoka 411-8540, Japan

Tel: 81-559-81-6855

Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BJ716634 MF01FFA CDNA Oryzias latipes CDNA clone MF01FFA013h19 3',
                                                                                                                                                   Contact: Mita K
Genome Research Group
National Institute of Agrobiological Sciences
Owashi 1-2, Tsukuba, Ibaraki 305-8634, Japan
Tel: 81-29-838-6120
Fax: 81-29-838-6120
Email: kmitue@nias.affrc.go.jp
                1 (bases 1 to 683)
Mita, K., Ishikawa, Y. and Yamauchi, M.
Establishment of cDNA database of medaka, Oryzias latipes
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68.7%; Score 20.6; DB 1; Length 683; 74.1%; Pred. No. 2.7e+02; ive 3; Mismatches 4; Indels
Beloniformes; Adrianichthyidae; Oryzinae; Oryzias
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db xref="taxon:8090"
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/dev stage="fry stage 40"
/clone_lib="MF01FFA CDNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ||:|| | ||||||:|||| ||:||
483 GCTACAAGGAGGATCATGAGCCTGT 509
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Oryzias latipes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'sex="female/male mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 GCUACGCGTAGAGCAUCATGATCCUGT 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: tshini@genes.nig.ac.jp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db xref="taxon:8090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tissue_type="brain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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1. .683
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      clone="br5670'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BJ716634
BJ716634.1 GI:45257475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 74.14
Local Similarity 74.14
Local Similarity 74.14
Local Similarity
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BJ716634/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEFINITION
                          REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
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VERSION
KEYWORDS
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AUTHORS
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JOURNAL
COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Ambystoma mexicanum"
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                                                                                                                                                   BL285D D03 6-Day Axolotl Tail Blastema (6DAxBL) Ambystoma mexicanum cDNA 5 similar to Unknown (protein for MGC:89099) (Xenopus tropicalis), mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AU170138 AU170138 CBJ bp mRNA linear EST 24-FEB-2005 AU170138 Ol-br-ad cDNA Oryzias latipes cDNA clone br5670, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Habermann, B., Bebin, A.G., Herklotz, S., Volkmer, M., Eckelt, K., Pehlke, K., Epperlein, H.H., Schackert, H.K., Wiebe, G. and Tanaka, E.M. An ambystoma mexicanum EST sequencing project: Analysis of 17,352 expressed sequence tags from embryonic and regenerating blastema cDNA libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oryzias latipes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii, Neopterygii; Teleostei; Euteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Ambýstoma mexicanum
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomatidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Max Planck Institute of Molecular Cell Biology and Genetics,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfotenhauerstrasse 108,01307 Dresden, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 0049 351 210 2620
Fax: 0049 351 210 1489
Email: tanakaempi-Jobg.de
Plate: BL285D row: 03 column: D
Seg primer: GCA CAT TAG GCC TAT TTA GGT GAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          230 GCTACACGAAGAGCGGCATGATCCTGT 256
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4 GCUACGCGTAGAGCAUCATGATCCUGT 30
                                                                                                                                                                                                                                                                                                                                                                                                                       Ambystoma mexicanum (axolot1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genome Biol. (2004) In press
Contact: Elly M. Tanaka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                     CO786247.1 GI:51002227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (bases 1 to 526)
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ORIGIN

TITLE

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Gaps

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Hominidae, Homo.
1 (bases 1 to 521)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Laurasiatheria, Carnivora, Fissipedia, Canidae,
                                                                                                                                                                                                                                                                                                                                                                                   Contact: Kirkness EF
The Institute for Genomic Research
Department of Bukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini,
tigr-gss-dog-17000335914549 Dog Library Canis familiaris genomic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence-tagged connectors: A sequence approach to mapping and
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HS 5043_B2_D11_T7_RPCI-11 Human Male BAC Library Homo sapiens
genomic_clone Plate=619 Col=22 Row=H, genomic survey sequence.
                                                                                                                                                                                                                                           frkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K.,
Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and
Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:9615"
/db_xref="taxon:9615"
/clone lib="bog Library"
/note="Site 1: BetXI; Libraries were prepared from peripheral blood"
                                                                                                                                                                                                                                                                                                                    The dog genome: survey sequencing and comparative analysis Science 301 (5641), 1898-1903 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
10449764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68.0%; Score 20.4; DB 9; Length 501; 70.0%; Pred. No. 3.1e+02; ive 3; Mismatches 6; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                High Throughput Sequencing Center
University of Washington
Voll Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Mahairas GG, Wallace JC, Hood L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'organism="Canis familiaris"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         263 CAGGCTAATGTTAGAGAATCATGATCCTTT 234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="genomic DNA"
/strain="Standard Poodle"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
1. .501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirknes@tigr.org
                         genomic survey sequence
                                            ČE251821
CE251821.1 GI:35948893
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AQ405865.1 GI:4415853
                                                                                                            Canis familiaris (dog)
Canis familiaris
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Best Local Similarity 70.0%
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Merazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Actinopterygii, Neopterygii, Teleostei, Euteleostei, Protacanthopterygii, Salmoniformes; Salmonidae, Oncorhynchus.

1 (Dases 1 to 451)
Govoroun, M., Guiguen, Y. and Le Gac, F.
Gonstruction and primary characterization of normalized cDNA libraries in rainbow trout, Oncorhynchus mykiss
Unpublished (2003)
On Apr 7, 2003 this sequence version replaced gi:29587474.

INRA - SCRIBE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone lib="tcay"
/note="Vector: pT7T3D-pac; Rainbow trout multi-tissues -
normalized + 1 subtraction (tcay); Clone distribution :
AGENAB Resource centre. Francois PIUMI,
Francois Piumi@jouy.inra.fr, IMRA, CEA Radiobiologie et
Etude du genome (LREG), Domaine de Vilvert, 78352,
Jouy-en-Josas cedex, France, +33 (0) 1.34.65.28.02, +33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: Yann.Guiguen@beaulieu.rennes.inra.fr
Sequence cleaned of vector, adaptator and repetitions. Contact us
at sigenasupport@jouy.inra.fr to obtain the chromatogram of this
                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="tcay0017b.e.20"
/tissue_type="adipose tissue, blood, brain,
differentiating gonads, gills, interrenal, intestine,
kidney, liver, muscle, ovary, pituitary, testis"
/lab_host="from embryos to adults"
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                     Length 724;
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Pred. No. 3.1e+02;
3; Mismatches 6; Indels
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                                                                    4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Campus de beaulieu, RENNES cedex, 35042, France
Tel: 02.23.48.50.09
Fax: 02.23.48.50.20
                     Score 20.6; DB 3;
Pred. No. 2.7e+02;
3; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
1. .451
/organism="Oncorhynchus mykiss"
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| CTGGCTACAGAAGAGCATCATGGCCCTGT 108
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                                                                                                                                                                                                                                                                                                                                                                                                           Oncorhynchus mykiss (rainbow trout) Oncorhynchus mykiss
                                                                                                                                        605 GCTACAAGGAGGATCATGAGCCTGT 579
                                                                                                            4 GCUACGCGTAGAGCAUCATGATCCUGT 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence.
Plate: 0017 row: e column: 20
Seq primer: M13F.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/db_xref="taxon:8022"
                                                                                                                                                                                                                                                                                                                                                                BX306829.2 GI:40223548
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70.0%;
                     ch 68.7%;
1 Similarity 74.1%;
20; Conservative 3
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Best Local 8
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FEATURES

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388 CAGGCCACGCGAAGAGCTGCTTAATCCTGT
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CC494201.1 GI:31806325
GSS.
                                                                                                                                                                                                  CA058120.1 GI:24388363
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Best Local Similarity
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CA058120/c
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                                                                                                                                                                                                                                                                                                                                                                 /Clone "lib="RPCI-11 Human Male BAC Library"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
Male blood DNA was isolated from one randomly chosen donor
and partially disested with a combination of EcoRI and
ECORI Methylase. Size selected DNA was cloned into the
pBACe3.6 vector at EcoRI sites"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AJ745356 ALIticum turgidum etiolated seedling 20 days old Triticum turgidum etiolated seedling 20 days old Triticum turgidum cDNA clone 05716R, mRNA sequence.
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Triticum turgidum
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooldeae; Triticeae; Triticum.
I (basea I to 631)
Cifarell, R.A., D'Onofrio,O. and Lauria,G.
Expressed Sequences Tags (ESTs) library from totipotent cDNA of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="etiolated seedling"
/dev_stage="20 days old"
/clone_llb="Triticum turgidum etiolated seedling 20 days
old"
Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.mad.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Resear h Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu
Plate: 619 row: H column: 22
Seq primmer: T7
Class: BAC ends
High quality sequence stop: 521.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 521;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 20.4; DB 9;
Pred. No. 3.2e+02;
2; Mismatches 6;
                                                                                                                                                                                                                                                                                   /mol_type="genomic_DNA"
/db_xref="taxon:9606"
/clone="Plate=619 Col=22 Row=H"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Triticum turgidum"
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                                                                                                                                                                                                                                           1. .521
/organism="Homo sapiens"
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/db_xref="taxon:4571"
/clone="05716R"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 73.3%;
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                    /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biotechnology
Metapontum Agrobios
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Unpublished (2003)
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Matches 23; Conservative
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KEYWORDS
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AJ745356/c
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1 CAGGCUACGCGTAGAGCAUCATGATCCUGT 30

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CH240 329KB.T7 CHORI-240 Bos taurus genomic clone CH240 329KB, genomic survey sequence.
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   EST 04-MAR-2003
                                                                                                                                                                                                                Eukaryotta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Proteacathopterygii; Salmoniformes; Salmonidae; Salmo.

1 (bases 1 to 639)

Rise, M.L., von Schalburg, K.R., Brown, G.D., Mawer, M.A., Devlin, Ruippers, N., Busby, M., Beetz-Sargent, M., Alberto, R., Gibbs, A.R., Smailus, D.E., Jones, S.J., Schein, J.B., Marra, M.A., Shukin, R., Zernik, J.A., Nelson, C., Jones, S.R., Butterfield, Y.S., Stott, J.M., Ng, S.H., Davidson, W.S. and Koop, B.F. Development and application of a salmonid EST database and cDNA microarray; data mining and interspecific hybridization
                                                                                                                                                                                                                                                                                                                                                        Devlin, R.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:8030"

/db_xref="taxon:8030"

/note="Wetor: pGMVsport6; Library Creator: Research

Genetics; Atlantic salmon tissue contributors: Carlo

Bagi, Mitch Uh and Robert Bevlin (DFO, Vancouver, B.C.),

Simon Jones (PBS, Nanaimo, B.C.), Seaspring Hatchery

(Crofton, B.C.), Rachel Roper (University of Victoria)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bos taurus
Bos taurus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genome Sciences Centre, BC Cancer Agency
CDNA preparation, sequencing and bioinformatics:
Sucerfield, R Kirkpatrick, J Asano, N Girn, R Guin, D Lee,
S Lee, T Olson, P Pandoh, A Prahbu, D Smailus, L Spence, J Stott,
S Taylor, G Yang, J Schein, S Jones and M Marra.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
CA058120 639 bp mRNA linear EST 04-
ssalrga513168 mixed_tissue Salmo salar cDNA, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14962987
Contact: Koop BF
Contrel for Biomedical Research
University of Victoria
DO BOX 3020 STN CSC, Victoria BC, V8W 3NS, Canada
Tel: 250 472 4075
Fax: 250 472 4075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              412 CTGGCTACAAGAAGAGCATCATGGCCCTGT 383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               characteristics
Genome Res. 14 (3), 478-490 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Salmo salar"
/mol_type="mRNA"
/strain="McConnell"
                                                                                                                                                              Salmo salar (Atlantic salmon)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VERSION
KEYWORDS
SOURCE
ORGANISM
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AUTHORS

REFERENCE

JOURNAL

COMMENT

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/Grond male and female"
// fissue_type="whole larva"
// fissue_type="whole larva"
// dev stage="1" day old larvae collected at Swarup Stage 30
// dev stage="2" day old larvae collected at Swarup Stage 30
// Embryol. Exp. Morphol 6: 373-383.1958)"
// lab_host="DH10B (T1 phage resistant)"
// clone_lib="stage-CtJ"
// clone_the indicated stickleback tissue, and a CDNA
library was constructed in the Express 1 plasmid vector by
Open Biosystems. First strand cDNA synthesis was primed
with an 54 bp linker primer containing an oligodT sequence
preceeded by a synthetic NoI site (first strand primer:
5'-GACTAGTTCTAGATCGGAGCGCGCCC(T)25-3'). Following
second strand synthesis, cDNAs were made blunt at the end
corresponding to the original 5 prime end of mRNA, and
cloned directionally into the NoI and EcoRV sites of
Express 1. Note that the EcoRV site is typically destroyed
in the blunt end cloning, leaving a junction of the form
// xxxATC (where is ATC is the second half of the EcoRV
site, and xxx is desived from the cDNA sequence). A map of
the Express 1 vector is available at interior fa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://www.openbiosystems.com/cdna_library_construction_fa_q.php#8 The primary_library_was_transformed_and_amplified_in_DH10B (Tl_phage_resistant)_bacteria. Clones available_from_Open_Biosystems:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gasterosteus aculeatus (three spined stickleback)
Gasterosteus aculeatus
Gasterosteus aculeatus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Metazoa; Chordata; Craniata; Vertebrata; Neoteleostei;
Actinopterygii; Neopterygii; Percomorpha; Gasterosteiformes;
Gasterosteidae; Gasterosteus.
1 (bases I to 131)
1 (bases I to 131)
2 (bases I to 131)
3 (chantz.j. and Myers, R.M.
Expressed sequence tags from Gasterosteus aculeatus
                                                                                                                                                                                                                                                                                                                                                                                                        /strain="Bitrufjordur marine sticklebacks, Iceland"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DN686483 11051 bp mRNA linear EST 30.
CGX47-C07.yld-s SHGC-CGX Gasterosteus aculeatus cDNA clone
CGX47-C07 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://www.openbiosystems.com/stickleback"
Contact: Grimwood, Jane
Stanford Human Genome Center
Stanford University School of Medicine
975 S. California Ave, Palo Alto, CA 94304, USA
Tel: 650 320 5917
Fax: 650 320 5801
Email: jane@ehgc.stanford.edu
                                                                                                                                                                                                                                                                                                                                                  organism="Gasterosteus aculeatus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:69293"
/clone="CLJ97-H05"
                                                                                                                                                                                                                                                        High quality sequence stop: E
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                        type="mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21; Conservative
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                                                                                                                                                                                                                                                                                                                        . .1332
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Best Local Similarity
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JOURNAL
COMMENT
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KEYWORDS
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                                                                                                                                                                                                                                                                                     FEATURES
               COMMENT
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Clones are derived from the bovine BAC library CHORI-240
(http://www.chori.org/bacpac/bovine240.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/ordering information.htm). This work
was undertaen as part of the International Bovine BAC Mapping
Consortium (IBBMC) by CSIRO Livestock Industries, Australia and the
British Columbia Genome Sciences Centre, Canada.
Beg primer: 17
Class: BAC ends.
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1 (bases 1 to 1332)
Kingsley, D.M., Peichel, C., Balabahdra, S., Grimwood, J., Dickson, M., Schmutz, J. and Myers, R.M.
Expressed sequence tags from Gasterosteus aculeatus
Unpublished (2003)
                                                                                         Holt, R., Stott, J., Yang, G., Barber, S., Smailus, D., Prabhu, A.-L., Tsai, M., Cloutier, A., Lee, D., Girn, N., Olson, T., Mayo, M., Tsai, M., Cloutier, A., Lee, D., Girn, N., Olson, T., Mayo, M., Kirkpatrick, R., Liu, J., Giln, R., Chan, A., Chiu, R., Mathewson, C., Wye, N., Mason, A., McMilliam, S., Barris, W., Boryme BAC End Sequences from Library CHORI-240, PLATES 294 to 398 Unpublished (2003)
Other GSSs: CH240_329K8.TARBAC13P2
         Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /sex="Wale" /
/sex="Wale" /
/clone lib="CHORI-240"
/note="Vector: pTARBACI.3; Site 1: Mbo1; Site 2: Mbo1;
Hereford bull Li Domino 99375; CHORI-240 Bovine BAC
library (Male) produced by Pieter de Jong"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                     The British Columbia Cancer Agency Genome Science Centre
600 W. 10th Ave, Vancouver, British Columbia, Canada V5Z 4E6
Tel: 604-877-6085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLJ97-H05.yld-s SHGC-CLJ Gasterosteus aculeatus CDNA clone CLJ97-H05 5', mRNA sequence.
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Gasterosteus aculeatus
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/strain="breed: Hereford"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Bos taurus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                db_xref="taxon:9913"
clone="CH240_329K8"
                                      Pecora; Bovidae; Bovinae; Bos.
1 (bases 1 to 759)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fax: 604-877-6276
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FEATURES

Query Match

Matches

DEFINITION

RESULT 11 DN711869 ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

JOURNAL

REFERENCE AUTHORS

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Gaps

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EST 30-MAR-2005

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975 S California Ave, Palo Alto, CA 94304, USA
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DN686482.1 GI:62035848
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DN686482/c
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                  /tissue type="aye" the page resistant)"
/dev stage="adult"
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/clone lib="SHGC-GGX"
/clone lib="SHGC-GGX"
/note="Vector: Express 1; Total and poly A+ RNA was isolated from the indicated stickleback tissue, and a cDNA library was constructed he Express 1 plasmid vector by open Biosystems. First strand cDNA synthesis was primed with an 54 bp linker primer containing an oligodT sequence preceded by a synthetic Not1 site (first strand primer: 5.cArTAGTTGAATGCGAGGCGCGCC(T(72=-3'). Following second strand synthesis, cDNAs were made blunt at the end corresponding to the original 5 prime end of mRNA, and cloned directionally into the Not1 and EcoRV sites of Express 1. Note that the EcoRV site is typically destroyed in the blunt end cloning, leaving a junction of the form 'xxxATC' (where is ATC is the second half of the EcoRV site, and xxx is derived from the cDNA sequence). A map of the Express 1 vector is available at:
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CLJ97-H05.X1d-t SHGC-CLJ Gasterosteus aculeatus cDNA clone
CLJ97-H05 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://www.openbiosystems.com/cdna_library_construction_fa
q.php#8 The primary library was transformed and amplified
in DH10B (T1 phage resistant) bacteria. Clones available
from Open Biosystems:
http://www.openbiosystems.com/stickleback"
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Gasterosteus aculeatus
Eukaryoteus aculeatus
Eukaryoterygii, Neopterygii, Teleostei; Euteleostei; Neoteleostei;
Aculnopterygii, Neopterygii; Percomorpha; Gasterosteiformes;
Gasterosteidae; Gasterosteus.

1 (bases 1 to 1372)
Kingsley, D.M., Peichel, C., Balabahdra, S., Grimwood, J., Dickson, M., Schmutz, J. and Myers, R.M.
Expressed sequence tags from Gasterosteus aculeatus
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                                                                                                                                                                                                                                                  /organism="Gasterosteus aculeatus"
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Stanford Human Genome Center
Stanford University School of Medicine
975 S California Ave, Palo Alto, CA 94304, USA
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Contact Grimwood, Jane
Crafford Human Genome Center
Stanford University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                  'sex="mixed male and female"
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                                                                                                                                                                                 High quality sequence stop: 834.
Location/Qualifiers
                                                                                                                             Email: jane@shgc.stanford.edu
Plate: 47
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                                                                           Tel: 650 320 5917
Fax: 650 320 5801
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/ Grown and the male "
/ (fissue_type="whole larva" |
/ (fissue_type="whole larva" |
/ (dev stage="1] day old larvae collected at Swarup Stage 30 |
/ (dev stage="1] day old larvae collected at Swarup Stage 30 |
/ (dev stage="1] day old larvae collected at Swarup Stage 30 |
/ (dev stage="1] day old larvae collected at Swarup Stage 30 |
/ (dev stage="1] day old larvae collected to the stage 30 |
/ (dev stage="1] day old larvae collected to the Express 1 plasmid vector by open Biosystems. First strand cDNA synthesis was primed of the marst be plasmid vector by open Biosystems. First strand cDNA synthesis was primed with an Stage by blinker primer containing an oligodr sequence preceeded by a synthetic NoI site (first strand primer: 5'-GACTAGTTCTAGATCGCAGCGCCCC(T) 25-3'). Following second strand synthesis, cDNAs were made blunt at the end corresponding to the original 5 prime end of mRNA, and cloned directionally into the NoI and ECORV sites of Express 1. Note that the ECORV site is typically destroyed in the blunt end cloning, leaving a junction of the form 'xxxxt' (where is ATC is the second half of the ECORV site, and xxx is derived from the cDNA sequence). A map of the Express 1 vector is available at:
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q.php#8 The primary library was transformed and amplified
in DH10B (T1 phage resistant) bacteria. Clones available
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                                                                                                                                                                                               /organism="Gasterosteus aculeatus"
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/mol_type="mRNA"
/db_xref="taxon:69293"
/clone="CLJ97-H05"
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                                                                                                                    High quality sequence stop: 843.
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Tel: 650 320 5917
Fax: 650 320 5801
Email: jane@shgc.stanford.edu
Plate: 97
                                                                                                                                            Location/Qualifiers
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source
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                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="eyes"
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/lab_host="Bh10B (TI) phage resistant)"
/lab_host="Bh10B (TI) phage resistant)"
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Rutinopterygii, Neopterygii; Teleostei; Buteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Gasterosteiformes;

Gasterosteidae; Gasterosteus.

E. (Dasses it ol 1669)

Kingsley, D., Grimwood, J., Dickson, M., Schmutz, J. and Myers, R.M.

Expressed sequence tags from Gasterosteus aculeatus
Unpublished (2004)

Contact: Grimwood, Jane Gasterosteus aculeatus
Contact: Grimwood, Medicine
Stanford University School of Medicine
Stanford University School of Medicine
975 S. California Avenue, Palo Alto, CA 94304, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://www.openbiosystems.com/cdna_library_construction_fa
q.php#8 The primary library was transformed and amplified
in DH10B (T1 phage resistant) bacteria. Clones available
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CH213-1N08.T7 CH213 Gasterosteus aculeatus genomic clone CH213-1N08
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                                                                                                                                                                                                                                      organism="Gasterosteus aculeatus"
                                                                                                                                                                                                                                                                                                                                                                                 'sex="mixed male and female"
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Tel: 650 320 5917
Fax: 650 320 5801
Email: jane@shgc.stanford.edu
Plate: 47
High quality sequence start: 15
High quality sequence stop: 782.
Location/Qualifiers
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Fax: 650 320 5801
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CL640951
LOCUS
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TITLE
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COMMENT
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                                                                                                                                                                                                            organism="Gasterosteus aculeatus"
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               Class: BAC ends
Class: BAC ends
High quality sequence start: 35
High quality sequence stop: 462.
Location/Qualifiers
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/db_xref="taxon:69293"
/clone="CH213-1N08"
Email: jane@shgc.stanford.edu
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Best Local Similarity 70.0
Matches 21, Conservative
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Search completed: January 8, 2006, 17:06:47 Job time : 2521 secs

